

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 18, 2003, 21:39:07 ; Search time 51 Seconds
(without alignments)
2371.562 Million cell updates/sec

Title: US-09-815-923-4
Perfect score: 3141
Sequence: 1 MPSPDAPPAPAPPPDLDPAT.....TIGREYVTSIPPADSLCNL 587

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
al number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp-archaea:*
2: sp-bacteria:*
3: sp-fungi:*
4: sp-human:*
5: sp-invertebrate:*
6: sp-mammal:*
7: sp-mhc:*
8: sp-organelle:*
9: sp-phage:*
10: sp-plant:*
11: sp-rodent:*
12: sp-virus:*
13: sp-vertebrate:*
14: sp-unclassified:*
15: sp-virus:*
16: sp-bacteriap:*
17: sp-archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2314	73.7	581	5	Q23969 drosophila
2	1681	53.5	631	6	Q9GMA5 ovls aries
3	1629.5	51.9	617	11	Q8R212 mus musculu
4	1618	51.5	576	5	Q9V7R0 drosophila
5	1615.5	51.4	631	5	Q9NB97 drosophila
6	1615.5	51.4	631	5	Q961H9 drosophila
7	1609.5	51.2	635	13	Q9DGN5 drosophila
8	1606	51.1	630	13	Q42482 rana catesb
9	1605.5	51.1	617	6	Q9MYW8 drosophila
10	1597.5	50.9	617	11	Q63380 macaca mula
11	1592	50.7	567	11	Q9WTR3 rattus norv
12	1592	50.7	597	11	Q9WTR3 rattus norv
13	1585.5	50.5	671	5	Q9NCTR4 caenorhabd
14	1579.5	50.3	671	5	Q963F3 caenorhabd
15	1573	50.1	629	13	Q902V1 brachydanio

17	1551	49.4	515	13	Q91802	Q918q2 coturnix co
18	1545	49.2	620	6	Q9GJ77	Q9GJt7 salmirl sci
19	1545	49.2	620	6	Q9GJ76	Q9GJt6 macaca fasc
20	1538	49.0	619	11	Q9J3J41	Q9J3J41 mus musculu
21	1538	49.0	620	6	Q9GJ75	Q9GJt5 salmirl sci
22	1533	48.8	619	11	Q9R0X6	Q9R0X6 mus musculu
23	1497	47.7	670	5	Q9SVZ4	Q9SVz4 trichoplusi
24	1448.5	46.1	572	6	Q9MYW7	Q9MYw7 macaca mula
25	1374.5	43.8	791	11	Q91Z02	Q91Zq2 mus musculu
26	1372	43.7	598	13	Q73771	Q73771 raja sp. ga
27	1360.5	43.3	598	13	Q91494	Q91494 torpeda cal
28	1340	42.7	629	13	Q9DE16	Q9DE16 oreochromis
29	1331.5	42.4	625	13	Q91BH6	Q91bh6 cyprinus ca
30	1302	41.5	597	5	Q25512	Q25512 manduca sex
31	1301.5	41.4	608	5	Q9NM10	Q9NM10 trichoplusi
32	1272.5	40.5	640	11	Q8VBW1	Q8VBw1 mus musculu
33	1269	40.4	622	13	Q91503	Q91503 torpeda mar
34	1256.5	40.0	611	13	Q91502	Q91502 torpeda mar
35	1247	39.7	621	11	Q91W12	Q91w12 mus musculu
36	1244	39.6	614	11	Q8VC9	Q8VC9 mus musculu
37	1227	39.1	638	11	Q9JMA9	Q9Jma9 mus musculu
38	1227	39.1	638	11	Q91Y60	Q91y60 mus musculu
39	1226	39.0	513	5	Q9V4E7	Q9V4e7 drosophila
40	1224	39.0	1201	5	Q9W1J0	Q9W1j0 drosophila
41	1221	38.9	638	11	Q9D317	Q9D317 mus musculu
42	1221	38.9	727	5	Q9U5A5	Q9U5a5 manduca sex
43	1215	38.7	602	4	Q8TCC2	Q8Tcc2 homo sapien
44	1211.5	38.6	943	5	Q02003	Q02003 drosophila
45	1211.5	38.6	943	5	Q9VR07	Q9VR07 drosophila

ALIGNMENTS

RESULT 1	Q23969	PRELIMINARY:	PRT:	581 AA.
ID	Q23969			
AC	Q23969			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	Cocaine-sensitive serotonin transporter.			
GN	SERT OR CG4545.			
OS	Drosophila melanogaster (Fruit fly).			
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OC	Ephydroidea; Drosophilidae; Drosophila.			
OX	NCBI_TaxID=7227;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Corey J.L., Quick M.W., Davidson N., Lester H.A., Guastella J.;			
RL	Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; U02296; AADI0615.1; .			
DR	FLYBase; FBgn0010414; SERT.			
DR	InterPro; IPR000175; Na/nttran_sympot.			
DR	Pfam; PF00209; SNF; 1			
DR	PRINTS; PR00176; NANBUSMPORT.			
DR	PRODom; PD000448; Na/nttran_sympot; 1.			
DR	PROSITE; PS00610; NA_NEUTROTAN_SYMP_1; 1.			
DR	PROSITE; PS00754; NA_NEUTROTAN_SYMP_2; 1.			
DR	PROSITE; PS0267; NA_NEUTROTAN_SYMP_3; 1.			
SQ	SEQUENCE 581 AA: 65177 MW: 1D39D07069C7CD2F CRC64;			
Query Match	73.7%;	Score 2314;	DB 5;	Length 581;
Best local Similarity	78.7%;	Pred. No. 2.1e-180;		
Matches 4/4;	Conservative 48;	Mismatches 63;	Indels 4;	Gaps 2;
QY	36 RQRETWAKKAEEFLAVVGAVDLGNWRREPYCYONGGAFLLPYVMLFFGLPLFEE 95			
DB	31 RRETEWGAKEFLAVIGFVAVDIGNWRREPYCYONGGAFLLPYVCLFLFGLPLFWE 90			
QY	96 LALGYHRCGCLTLWRIKRICPAKGVGYAICMIDIVYGMVYNTIIGAVYLLASLASIS 155			

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Db      91  LALGCFHRCGCLSIWKRICPALKGVAHICLIDYMGWYNTIIGMAVYVL--FASFTS 147
Qy      156  VLPWTSQCDNEBMTPLCTPVTSPOQNPNSNSTPAKEFEERNVLQHKNSGLDMGIRKSLA 2151
Db      148  KLPWTSQCDNPWNTNEMOQVTSNETFELTSLPAKEFEERKVLSEYKSGNGLDMGVPKPTLA 2078
Qy      216  LCVFGEFVLYVFSLIMKGVRSACKVYVWVWALAPYVLLLLRGLTPGATEGIRYVLTPE 2757
Db      208  LCVFGEFVLYVFSLIMKGVRSACKVYVWVWALAPYVLLIILLKGVSLPGADGCIKRYVLTPE 2678
Qy      276  MHLKNSKWIDAASQIFFSLCPGEGTLLALSNNKFNNNCYRDALITSSINCLTSLFAG 3355
Db      268  MHLKNSKWIDAASQIFFSLCPGEGTLLALSNNKFNNNCYRDALITSSINCLTSLFAG 3278
Qy      336  FVTFVSVLGVNAHQNKSIENGLDEBPGVLYFYPPAINTMGSGFMAIIFPLMLITIGLD 3958
Db      328  FVTFVSVLGVNAHQKSIDKVLDEBPGVLYFYPPAINTMGSGFVWSIIFPLMLITIGLD 3878
Qy      396  STFGGLEAVYATLALCDEYPRVLGRHREVEFAVLLLEIYICALPTTYGGVYVLDLANYGP 4455
Db      388  STFGGLEAMITLALCDEYPRVIGRRRLDVLILLATIFLICALPTMYGGVYVNLNLYGP 4427
Qy      456  GLAILFVVEPAEAGVCWYGVDRFESDEYKTLGHTPGFMWRTCSYISPVFLVLFVFSV 5151
Db      448  GLAILFVVEAAGVFMFGYVDRFESDEYQMLGSRGLFMRICMTYISPVFLTIFFSI 5078
Qy      516  LAHEMLGGEYTPMSISIVGWVMTGTYSCLPIYIIKLLI-IPGNCINIKITQPRE 573
Db      508  MGRKEMLGEYTPPMSISIVGWVMTGTYSCLPIYIIKLLI-IPGNCINIKITQPRE 566

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RESULT 2	09GMA5	PRELIMINARY:	PRT:	631 AA.
AC	09GMA5			
DT	01-MAR-2001 (Tremblrel, 16, Created)			
DT	01-MAR-2001 (Tremblrel, 16, last sequence update)			
DT	01-JUN-2002 (Tremblrel, 21, last annotation update)			
DE	Secotonin transporter.			
OS	Ovis aries (Sheep).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Caprinae; Ovis.			
OX	NCBI_TaxID=9940;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97259585; Pubmed=9105686;			
	Pedbury J.F., Tseng Y.T., McConnigal B., Penado K., Stephan M.,			
	Rudnick G.,			
	*Placental diogenic amine transporters: cloning and expression.";			
RL	Brain Res. Mol. Brain Res. 45:163-168(1997).			
RN	[2]			
RN	SEQUENCE FROM N.A.			
RP	Tseng Y.-T., McConnigal B.;			
RL	Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.			
RL	EMBL: AF246893; AAC01287.1; -			
DR	InterPro: IPR002437; 5HT_transporter.			
DR	InterPro: IPR000175; Na/ntan_symport.			
DR	Pfam: PF03491; 5HT_transporter; 1.			
DR	Pfam: PF00209; SNF; 1.			
DR	PRINTS: PR00176; NANESMPORT.			
DR	ProDom: PD00448; Na/ntan_symport; 1.			
DR	PROSITE: PS00610; NA_NEUTROTAN_SYM_1; 1.			
DR	PROSITE: PS00754; NA_NEUTROTAN_SYM_2; 1.			
DR	PROSITE: PSS0267; NA_NEUTROTAN_SYM_3; 1.			
Q0	SEQUENCE 631 AA; 70521 MW; 3fCB9A9385B2C8B3 CRC64;			

Query Match	53.5%	Score 1681	DB 6	Length 631
Best Local Similarity	53.2%	Pred. NO. 9.8e-129		
Matches 309; Conservative	103;	Mismatches 153;	Indels 16;	Gaps 7;
Oy	6 APPPTA---PPDLPATTAAKSRVVVSLTPARORETWAKAEFLLVAGCAVDLGNW	62		
	: : : :			

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Db      49  AVPNPGAGDOTHSPAAFT---ALVAEVRH-ERETWGKKVDFLLSVIGAVDGNW 103
OY      63  RPPYICYONGGAFELIPYCVMLLEGGELFLEIALGOYHRCGLTLMKRICPALGVCY 122
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      104  RPPYICYONGGAFELIPYIMAFEGIPLEFYMEPLGGOYHHRNGCISWTICPILFGIC 163
OY      123  AICMIDYMGMYNTIIGAVVYLLASLASINSVLPMTSCDKNENFPLCPYPSPOINP- 181
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      164  AICLIEFYIASYNTTMAVALYYLL--SSFTBOPLMTSCENSWNTGCTNVPSEDNITW 220
OY      182  --NSSPPEKEFERENVLEOHKNSGLDDMGPIKPSLALCEVFVFLVYFSLMKGVSAGKY 239
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      221  MLHSTSAEEFYRHHVLOHRSKGLDGLGSLMOLVLCIMLFIITIFYSTMKGVKTSKV 280
OY      240  VWYATALAPYVLLILLRGVLLPGATEGIRYLLPEMHKLONSKVMIDASQIFSLGPG 299
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      281  VWYATFPYIILLILLRGATLPGMARGVFLYFKPMOKLLETGVMWVDAAOIFSSLGPG 340
OY      300  FGLLLLSSTNKNNNCYDALITSSINCITSLFAGFYIESVLGYMAHVONKSLIEPGL 359
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      341  FGVLLEFASYNKHNHCYDALVTSVYNCKMSPFSGVFLFYVLGYMAEMKREDVSEVAKD 400
OY      360  -GGGLFVYVPELIATMTGVSFMALIFPLMLITGLDSTFEGLEAVNTALCDEYPRVLR 418
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      401  AGSGLFETIYAEIANNMPASTFAFFELMLITLGLDFTFAGLRCGVITAYVADDEPHYMAK 460
OY      419  HREVFVAVLLLFYICALPPTTYGGVYVLDLINVGPGLALFVFVAAGVGVAVGVDR 478
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      461  RRENFVYGVVITCFPSLVTLPFGGAYVVKLLEEFATGPALVTAALLEAVAVFPGVINO 520
OY      479  FSEVDRTMGLHGFQMFWRTCMSYIESVPLLLEVFVSVAHEEMLGGEYTPSWSTYGV 538
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      521  FCLDIVEKMLCFSGFMWKICWVAISPLFLFIFICSFLMSPPQLRFRYDPRWMSIILGYC 580
OY      539  MGTGVYSCIPLYIYKLLTTPGNCJNR-IKTIQREYVSI 578
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      581  IGTSSEFCIPYIYVLLVTPGLTERIKIIGITKPTTPE 621

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RESULT 3
08R212
ID 08R212 PRELIMINARY; PRT; 617 AA.
AC 08R212;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Norepinephrine transporter.
GN SLC6A2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=PLACENTA;
RA Loebbe S.Y., Bonisch H., Bruss M.;
RT "Molecular cloning and functional expression of the murine
RT norepinephrine transporter cDNA.";
RL Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
DB EMBL; AJ439987; CAD29195.1;
SQ SEQUENCE 617 AA; 69227 MW; 591641246b8f759c CRC64;

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	Query Match	51.98;	Score 1629.5;	DB 11;	Length 617;
	Best Local Similarity	52.18;	Pred. No. 1.5e-124;		
	Matches 310; Conservative	104;	Mismatches 154;	Indels 27;	Gaps 9
OY	1 MPESDAPRATAPP-----PDLPATTAQ-----KSRSVVSL-----TPARORETMAAKAEF	47			
Dd	6 MNPQVPELGADPLPECPRLPCCKTADTLIVKERNGVCCLLASODSDAOPRETGGKKIDF	65			
OY	48 LLAVGFADVLDGNWMEFPITCYONGSGAFILPYCMILLFGSLPFLELALGOYNHGCGL	107			
Dd	66 LLSVGFAVDLLAWNMFEPYLCTKNCGSGAFILRYTFELTIACMPLFYEMLALGOYNREGGA	125			

OY 108 TLNKRICPALKGVYALCMIDYMGVYNTTIGMAYVYLLASINSVLPMTSCDQEW 167
126 TVMK-ICPEFKGVYALVIALVYGYNTIAMSLLTFRSP-TLN--LPMNCGSHN 181
OY 168 TPLCT-----PVTSPT--NPNSSTPAKEFFERNVLEOHKSNGLDMGPPIKPSALCV 218
182 SPNCTDPLKLNASVLDGHTKYSKKKPPAPAEFERGVLLHHESSGIDHIGPOMQLLCL 241
OY 219 FGCVLVYFSLMKVBSAGVWVWTLAPVYVLLILARVYLLPGATEGRIRYITPBMKH 278
242 MVYIVLVYFSLMKGVKTSKVWVWTLAPVYVLLVHGVYLLPGACNGINAYLHIDFYR 301
OY 279 LQNSKVIDAASQIFSLGPGFTLLASYNKNKNNDYDALITSSINCLTSPLAGFVI 338
302 LKERTVIDAATQIFSLGPGFTLLASYNKNKNNDYDALITSSINCLTSPLAGFVI 361
OY 339 FSVLVYMAVONKSIEVEGLEPGLVRYVYPAIATMGSEVMAIIFPLMLITGLDSTF 398
362 FSLIGVMAHEKVNIEDVATEGAGLVYILPEASTLSGSEPMVAVLEFLMALGLDSSM 421
OY 399 GGLVAVTALCDEYPRVLRHREYFVAVLLFIYICLPPTTGGVYVLDLNVYGGCLA 458
422 GGMVAVITGLADP-OVLKRHRKLTCTCVVITSTFLALFCITKGIYVLELDTFAAGTS 480
OY 459 ILFVFEAAGVGVGVDFRSEEDVFTMLGHTPGMFWRTQMSYISPEVLLVFEVSLAH 518
481 ILFVFEAAGVGVGVDFRSEEDVFTMLGHTPGMFWRTQMSYISPEVLLVFEVSLAH 540
OY 519 EEMLGERTYPSWSTIVGVMWGTGTVSCIPLYIYIKLLTPGNCINIKTIORPE 573
541 KPLTYDDTYTPPMANVMYGMIALSSMLVPAVYIKFSLRSGLMERVAAGITPE 595

RESULT 4

OY 09V7R0 PRELIMINARY; PRT; 576 AA.
AC 09V7R0; DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE CG8380 protein.
GN DAT OR CG8380.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
EN 11
SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA MEDLINE=20196006; PubMed=10731137;
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanalides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews Pannkuch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Butler H., Cadieu E., Center A., Chandra I.,
RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodet A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Moutlov G., Mishina N.V., Mobarry C., Morris J., Moshnell A.,
RA Moutlov G., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.C.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siedman Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RA "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL: AE003806; AAF57986.1;
DR Flybase: FBgn0034136; DAT.
DR InterPro: IPR000175; Na/nttran_sympoort.
DR Pfam: PF00209; SNF.1.
DR PRINTS: PR00176; NANEUSMPORT.
DR PRODOM: PD000448; Na/nttran_sympoort.1.
DR PROSITE: PS00610; NA_NEUROTRAN_symp_1; 1.
DR PROSITE: PS50267; NA_NEUROTRAN_symp_3; 1.
SO SEQUENCE 576 AA; 64302 MM; 0360B72FE57F909 CRC64;

Query Match 51.5%; Score 1618; DB 5; Length 576;
Best Local Similarity 54.5%; Pred. No. 1,26-123;
Matches 292; Conservative 96; Mismatches 128; Indels 20; Caps 4;

OY 37 ORETMARKEFLAVAGVADLVGMVRRPYTCYONGGAPLIPCVMLLFGCLPFLTEL 96
26 ERETWSKRVDSLVSIGFADLVANVRPPLYCYRNGGALVPGIMLVGGIPLEFMEL 85
OY 97 ALGOYHRCGLTLNKRICPALKGVYALCMIDYMGVYNTTIGMAYVYLLASINSV 156
86 ALGONHNRKGAITCGRLVPLEFGIGVAVVLAIFVDPYVYNTIAMSLLRFPAST--NS- 142
OY 157 LPTSCNENMTPLCTVYTSPTNPNSSTPAKEFFERNVLEOHKSNGLDMGPPIKPSAL 216
143 LPTSCNENMTPLCTVYTSPTNPNSSTPAKEFFERNVLEOHKSNGLDMGPPIKPSAL 186
OY 217 CVFVFLVYFSLMKVBSAGVWVWTLAPVYVLLILARVYLLPGATEGRIRYITPBMKH 276
187 CLLIVYICFSLMKVBSAGVWVWTLAPVYVLLILARVYLLPGATEGRIRYITPBMKH 246
OY 277 HKLQNSKVIDAASQIFSLGPGFTLLASYNKNKNNDYDALITSSINCLTSPLAGFVI 336
247 SAIKAEVWDAATQIFSLGPGFTLLASYNKNKNNDYDALITSSINCLTSPLAGFVI 306
OY 337 VIFSVLGMVMAVONKSIEVEGLEPGLVRYVYPAIATMGSEVMAIIFPLMLITGLDSTF 396
307 VIFSVLGMVMAVONKSIEVEGLEPGLVRYVYPAIATMGSEVMAIIFPLMLITGLDSTF 366
OY 397 TFGLEAVTALCDEYPRVLRHREYFVAVLLFIYICLPPTTGGVYVLDLNVYGGCLA 456
367 SFGSEAVITRLALDEPKIT-KRNELEVAGLFSLYFVAGLASCIOGGFTFFHLDRAAG 425
OY 457 LAILVFAEAGVGVGVDFRSEEDVFTMLGHTPGMFWRTQMSYISPEVLLVFEVSLAH 516
426 YSLVAVFAEAGVGVGVDFRSEEDVFTMLGHTPGMFWRTQMSYISPEVLLVFEVSLAH 485
OY 517 AHEMLGERTYPSWSTIVGVMWGTGTVSCIPLYIYIKLLTPGNCINIKTIORPE 572
486 GYEPLTYDDTYTPPMANVMYGMIALSSMLVPAVYIKFSLRSGLMERVAAGITPE 541
RESULT 5
OY 09NB97 PRELIMINARY; PRT; 631 AA.
AC 09NB97; DT 01-OCT-2000 (TREMblrel. 15, Created)

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DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE Dopamine transporter.
CN DAT OR CG8380.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidae; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEAD;
RA Porzgen P., Sonders M.S., Reed A.I., Ingram S.L., Amara S.G.;
RT "Identification of neurotransmitter transporters from Drosophila
  melanogaster.";
RL Abstr. - Soc. Neurosci. 25:160-160(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=HEAD;
RA Porzgen P., Park S.K., Hirsh J., Sonders M.S., Amara S.G.;
RT "An antidepressant-sensitive dopamine transporter from Drosophila
  melanogaster.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
EMBL: AF260833; AAF76882.1; -.
FLYBase: FBgn0034136; DAT.
DR InterPro: IPR000175; Na/nttran_symport.
DR Pfam: PF00209; SNE. 1.
DR PRINTS: PR00176; NANEUSMPORT.
DR PRODOM: PD000448; Na/nttran_symport; 1.
DR PROSITE: PS00610; NA_NEUOTRAN_SYMPT_1; 1.
DR PROSITE: PS0267; NA_NEUOTRAN_SYMPT_3; 1.
SQ SEQUENCE 631 AA; 70349 MW; AAF3B53F5A91ED89 CRC64;

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Query Match	51.4%	Score 1615.5	DB 5	Length 631
Best Local Similarity	51.5%	Pred. No. 2.2e-123		
Matches	296	Conservative 99	Mismatches 137	Indels 43
				Gaps 5
QY	37	QRETWARKAEFLAVGFAVDLGNVWREPRYICYONGGGAFLIPYCVMLFGPLFLEL	96	
Db	26	ERETMSKQVDPELLSVIGFAVDLAWVWREPRYLCKRNGGAFLVPYGMVLVGIPLEYNEL	85	
QY	97	ALGQYHHCGLITLMKRLCPALKGVAICMDITMGATNTITIGMAVYLLIASLASTNSV	156	
Db	86	ALGGHNRKGAITCGRLVPLEFGIGAVALLAIFYVDFEYNYIAMSLEFFPASEFT--NS-	142	
QY	157	LPMTSCNENMTPLCTPYTSP-----	184	
Db	143	LPMTSCNINMTPCRPESQNASRVPYIGYISDLYAMGNOSLYNETIYMGSSLDITSAV	202	
QY	185	-----TPAKEEFERNVLEQHKSGNDLMDGPIKPSALCYGVFLVFSFLMKGVRSAG	237	
Db	203	GHWGFSQASAEYENRYILELRSEGHIDIGAIKMDALCLLIYLLCYFSLMKGISNSG	262	
QY	238	KVWVNTALAPRVVLLILLARGVTLPGATEGIRYTLTPEMAHLQNSKYMIDAASQIFPSLG	297	
Db	263	KVWVFETALFPYAVLLILLIRGLTLPGLSGLIQYLLTPNFSAIYKAAEAWVDAATQVFFSLG	322	
QY	298	PGFSTLLASSYNFKFNNNCYRDALITSSINSITFSLAGEVYFSLGVMAHONKSIEPVG	357	
Db	323	PGFVLLAYASYNKHNNYKDALITSFINSATSFIAQVYFSLGVMAHNLGYRIEDVA	382	
QY	358	LESGDLVFIYPEAIATMTGSVFMAIIFELMLTILGDSITFGGLEAVTALCDEYPRVLG	417	
Db	383	TEGGLGVFVYVPAIATMTPASTFMALLFFPMMLTLIGDSSRFGSEAIITLALSDPEPK-K	441	
QY	418	RHRVEFPAVLLFIYICALPTTYGGYLVLDLWVYGBGLAILEVFAEAAAGVCWGYVD	477	
Db	442	RNRELFAVAGLESLFVNVGLASCTGGGCFEYFHLDRYAAGYSIIIAVFEFAIVSMIYGTN	501	
QY	478	RFSEDVETMLGHPRGFMFCWQSYISPELTLVLVFSLIAHEEMLGGEYTPMSISYNG	537	
Db	502	RFSDDIDMGHPGRGWQCMREVAIPLEFLITVYGIGIEPLTADYVPSMANALGW	561	

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QY      538 VMGTGVSCDPLYYIKLLITPNCINRIKTIQRP 572
      : : : | | | : | | | : |
Db      562 CIAGSSVVMIPAVAFIKLLSTPESLRQRFTLLTP 596
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RESULT 6			
ID	Q961H9	PRELIMINARY:	PRT: 631 AA.
AC	Q961H9		
DT	01-DEC-2001 (TReMBLrel. 19, Created)		
DT	01-DEC-2001 (TReMBLrel. 19, Last sequence update)		
DT	01-JUN-2002 (TReMBLrel. 21, Last annotation update)		
DE	GHZ9292p (Dopamine transporter).		
GN	DAT OR CG8380.		
OS	Drosophila melanogaster (Fruit fly).		
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;		
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OC	Ephydroidea; Drosophilidae; Drosophila.		
OX	NCBI_TaxID=7227;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=BERKELEY:		
RA	Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,		
RA	Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,		
RA	Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,		
RA	Nunoo J., Paolel J., Paragas V., Park S., Phouanavong S., Wan K.,		
RA	Yu C., Lewis S.E., Rubin G.M., Celniker S.;		
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.		
RT			

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RP SEQUENCE FROM N.A.
RA Gu H.H., Wu X.;
RT "Phenylalanine 105 in transmembrane domain 2 of the dopamine
RL transporter is involved in cocaine binding.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY051579; AAK93003.1; -
DR EMBL; AF439752; AAL52055.1; -
DR FlyBase; FBgn0034136; DAT.
DR InterPro; IPR000175; Na/nttran_symport.
DR Pfam; PF00209; SNF; 1.
DR ProDom; PD000448; Na/nttran_symport; 1.
DR PROSITE; PS00610; NA_NEUROTTRAN_SYM_1; UNKNOWN_1.
DR PROSITE; PS50267; NA_NEUROTTRAN_SYM_3; 1.
50 SEQUENCE 631 AA; 70330 MW; E7582D17F81E31E6 CRC64;

Query Match          51.4%: Score 1615.5; DB 5; Length 631;
Best Local Similarity 51.5%: Pred. No. 2.2e-13;
Matches 296; Conservative 99; Mismatches 137; Indels 43; Gaps 5;

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QY 37 QRETMARKAEEELLAVNGEPAVDLVGMWHPPTCYXONGGAFILIPCYMLLEGGJLPFLEL 96
Db 26 ERETTMSKRVDLVLISVIGPAVDLAVWMRRPYLYCTKNGGAFVLPYIGIMLVGGJLPFMYEL 85
QY 97 ALGQYAHNGCGCLTLLKRLICPALKGVAICMIDIMGMWNYTIIOMAVYLYLASLASINSV 156
Db 86 ALGQHNNKGAITTCGRGLVPLEKGIYAVNVLIAFYVDYYINVIIMSRLRFFPAST--NS- 142
QY 157 LPMTSCNENWNTPLCTPVTSP-----OTNPNS----- 184
Db 143 LPMTSCNNINWNTPCRPFESONASRAVPVIGNYSDLYAMGNOSLLYNETMYNGSSLDTSAY 202
QY 185 -----TPAKEFERFERNVLEOHKSNGLDDMGPIKPSIALCEYGFVLYVYSLKKGVRSAG 237
Db 203 GHVEGFQSAASEYFNRIYLELNRSEGHJHDGALIMDAALCLLIYLLCYCFSLMKGIPTSG 262
QY 238 KVVWVNTALAPVYVLLIILARGVTLPGATEGIRYVLPPEMKLONSKWIDAASOIFPSLG 297
Db 263 KVVWFIALPFAVLLIILIRGLIPLGSLGIQYILTFNFSATIKAEWVMDAATVDFPSLG 322
QY 298 PGEFTLLALSSYNKFNKNNCYRDALITSSINCILTSFLAGFYVSVLGMAHYONKSIFEVG 357
Db 323 PGCFVLLAYKSYKNYHNHYKDALITLSPINSATSPFIAGFYVSVLGMAMHTLGVRIEDVA 382
QY 358 LGGGGLVFIYPEAIATMTGSVFMAILLMLTLTGLDSTFGGLEAVTALACDEYPRVLG 417

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[illegible]

Oy		336	VIVSVSLGVMAHYGNKSSIEEVGLGGPGVLFVYVEAATNTMGSFMAIIFLMTLTGID	395
Dd		377	FAISILIGVMAHEHKVKIEDVATGAGVFLITYPEALISTSGSTFMVAFFIMLTGID	436
Oy		396	STFGLEAVTALCDEYPRVVGRRHREVEAAVLLEIFYICALPTTYGGVYLVDLNVGP	455
Dd		437	SSMGMEVITIGLADDF-HILKKORHKTLPFGVSFTGLTFALFCITNGIYVLTILDTRFA	495
Oy		456	GLAILEVFVAEACVCVVYQDRFSEDRYTMLGHTPGMFWMTCSYSISPVLVLEVRSV	515
Dd		496	GTSILFVLMALCAIVSMFYGDRESIDIQQMMCKRPGCLWRLCKWFSPAFLEPVI	555
Oy		516	LAEHMDAGEETVYSWSITGVWMVGTSCVISPIYIKLLITPGNCIRKTIQRPE	573
Dd		556	INFRPLYDDTYTFPFPMARIGMALSLMLLVPAIVYIKEMVNRKTERELAYCTIRE	613
<hr/>				
RESULT 8				
ID	: 042482	PRELIMINARY:	PRT:	630 AA.
AC	042482:			
DT	01-JAN-1998 (TREMBLrel_05, Created)			
DT	01-JAN-1998 (TREMBLrel_05, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel_21, Last annotation update)			
De	L-phlephrine transporter.			
OS	Rana catesbeiana (Bull. frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OX	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.			
RN	NCBI_taxid=8400;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=SYMPATHETIC GANGLION:			
RX	MEDLINE=97248649; PubMed=9092590;			
RA	Apparisundaram S., Moore K.R., Malone M.D., Hartzell H.C.,			
RA	Blakeley R.D.;			
RT	"Molecular cloning and characterization of an L-epinephrine			
RT	transporter from sympathetic ganglia of the bullfrog, Rana			
RT	catesbeiana.";			
RL	J. Neurosci. 17:2691-2702(1997).			
DR	EMBL, U72877; AAB67676.1; -			
DR	InterPro: IPR000175; Na/ntraa_sympor.			
DR	pfam: PF00209; SNF: 1.			
DR	PRINTS: PR00176; NANEUSMPOT.			
DR	Prodrom: PD000448; Na/ntraa_sympor: 1.			
DR	PROSITE: PS00610; NA_NEUROTTRAN_SYMP_2; 1.			
DR	PROSITE: PS00754; NA_NEUROTTRAN_SYMP_2; 1.			
DR	PROSITE: PS50267; NA_NEUROTTRAN_SYMP_3; 1.			
SO	SEQUENCE 630 AA; 70928 MW; 4FZA06556DC956C6 CRC64;			
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Query Match 51.1%; Score 1606; DB 13; Length 630:				
Best Local Similarity 51.1%; Pred. No. 1.3e-122;				
Matches 285; Conservative 106; Mismatches 153; Indels 14; Gaps 4				
Oy		25	SRSVYVSLTPARORETNAKKAEFLLAVVGAFAVDLGNNWRFPYICYONGGAFLLPYCYML	84
Dd		56	SQKEVEVPREDQERHMKKIDILLSSVGFSDLANVRFPYLYCKNGGAFLLPYTLFL	115
Oy		85	LFGLPLPFEFLDALGOYHRCCGLTLMKKICPAKKGVAICAIMIDIMYGNYTTTGMAVY	144
Dd		116	IIAAGPLRYMELALGOYNREGCAIPWK-ICDPFKGVGYTVLIILVAFYYNIILAMSIX	174
Oy		145	YLIASLASINEVLPTSCDNEBNPPLCIPVT-----SPQTNPNSSTPAKKEFFERNV	195
Dd		175	YL----ASSFTSELPRTTCGANNPNPCNDPILLANSFPGNGTKSKYKLYLTPAQTRYEBV	231
Oy		196	LEOHKSGLDMGRIPKPSLALCEGVFNLYVYFSLMKGVASGAKVVMYTALAPYVLLLL	255
Dd		232	LHLHSAGSIHDGLGRMQTLCTCLFAVLIIVLFESLMKWGKTSQKVWIMATPIPVVLFVL	291
Oy		256	ARGVTLPCATGCIKYILLTPENHKDKNSKVVIDASAQIFPSLCPGCGTLLALLSYKFEKN	315
Dd		292	IRGVTLPPSEGSIAVYLIHIDRKLRPEKVMIDAAOIFYSLGAGGVLIATAFASVYKFDNN	351

	Matches	307:	Conservative	106:	Mismatches	155:	Indels	27:	Gaps	10:
QY	1	MPSPDAPP---	APPAAPPDPLPA-TTAAQ----	KSSSVSVSLT----	PARORETMAKAAEF	47				
Db	6	MNPQVQPPENNMGADTGP	EQPRLRAKRTAE	LLVYKERNKGVOCLAPR	GDGAOPRETTGKKIDF	65				
QY	48	LLAVYGFVAVDIGNVWRPFYICYONGGGAFLL	PRYCVMLLFGLPLPFLELALAGVHRCGL	107						
Db	66	LLSYVGFVAVDLANWRPFYLCYKNGGAFLL	PLYLLFIAGMPLFYMBLALGOVNRREGAA	125						
QY	108	TLMKRICPALKGVGVAICIMIDITMGMYNTIT	IGNAVUYLLIASLASINSVLPWTS	CDNEMN	167					
Db	126	TYWK-ICPFPGGVGVAIVALLIAYLGYFYNNV	IASLSYLLSESSF-TLN--LPWTDCGHTWN	181						
QY	168	TPICLT-----	PPTSPTQ--NPNSSPAKFEFFERNVLE	EOHKSNGSLDDMGPIKPSALCY	218					
Db	182	SNPCDPEKPLNGSVLGNNHTKYSKKEFTFPA	EEYERGVHLHSESGIHDI	GLPOMQLLCL	241					
QY	219	FGVEPLVYFESLMKGVSAGKVVWYVYVYVY	LLALAPVYVLLILALRGVYLTLP	GATEGIRYVYLTPEPMK	278					
Db	242	MVVYVILFESLMKGKTKSGKVYVMTATLP	RYEVLEVLLVHGVTLRGASGINAVYLHIDF	RYR	301					
QY	279	LQNSKVVYIDAAASQIFPSLGGPFGILLAL	SSNKRNNNCYRALTLTSSINCILSTSLAGVI	338						
Db	302	LKEAVYIDAAATQIFESLGAEGVGLVIA	SVASYNKDDNCCYRALTLTSSINCTSFEVSGFAI	361						
QY	339	FSVLGYVMHAYONKSTEEVGLGPGGLVF	YVEYDEAATMGSEVMAITIFLMITTG	LDSTF	398					
Db	362	FSILGYMAHEKVNIEDVATGAGAVFLY	LEALISTLGSIFPMNAVFFVYMLALAGLDDSM	421						
QY	399	GGLEAVTTALCDEYPRVLGRHREVFVAV	LLFIYICALPTTYGCVYLVLDLNVY	PGCLA	458					
Db	422	GGMEAVITIGLADDF-QVLRHRRKRLFT	FGVTFSTFLALFCTYKGIYVLLTLDP	FAAGTS	480					
QY	459	ILFVYFAACVACVWYGVDRFSEVRYTM	LGHTPGMENMTCSYSLPFLVLPF	SVYLAH	518					
Db	481	ILFVYFAACVACVWYGVDRFSEVRYTM	LGHTPGMENMTCSYSLPFLVLPF	SVYLAH	518					
QY	519	EMLGEYTPSWSTYTGVMWGTGTTC	SCIPRYIYIKLLITPGNCINRIKTI	QIOPRE	573					
Db	541	KPLTYDDYIFPPMAWVGWGLIALSSMVL	VPYIVYIKFLSTGSIEMERLAVGITPE	595						
RESULT 10										
Q9MYW8										
ID	Q9MYW8	PRELIMINARY:	PRT:	617	AA.					
AC	Q9MYW8:									
DT	01-OCT-2000 (TREMBLrel. 15, Created)									
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)									
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)									
DE	Norepinephrine transporter.									
OS	Macaca mulatta (Rhesus macaque).									
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;									
OC	Cercopitheidae; Macaca.									
OX	NCBI_TaxID=9544;									
RN	[1]									
RP	SEQUENCE FROM N.A.									
RC	TISSUE=LOCUS COERULEUS;									
RT	Miller G.M., Madras B.K.;									
RT	"Cloning of dopamine, norepinephrine and serotonin transporters from									
RT	monkey brain."									
RL	Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.									
DR	EMBL, AF286026; AAF97251.1; -									
DR	InterPro: IPR001175; Na/nttra_synport.									
DR	Pfam: PF00209; SNF; 1.									
DR	PRINTS: PR001176; NANEUSPORT.									
DR	Prodom: PD000448; Na/nttra_synport; 1.									
DR	PROSITE: PS00754; NA_NEUOTRAN_SYM_2; 1.									
DR	PROSITE: PS50267; NA_NEUOTRAN_SYM_3; 1.									
SO	SEQUENCE	617	AA:	69245	MM;	FC6785F4454B76D3	CRC64;			

RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE-99069613; PubMed-9851916;
RA None;
RT "Genome sequence of the nematode *C. elegans*: a platform for
investigating biology. The *C. elegans* Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA "Tin Wollam A., Becker M., Graves T.";
RT "The sequence of *C. elegans* cosmid Y34E10B.";
RL Submitted (Mar-2000) to the EMBL/Genbank/DBJ databases.
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA "Waterston R.";
RT "Direct Submission.";
Submitted (Aug-2001) to the EMBL/Genbank/DBJ databases.
EMBL: AC024812; AAF59549.2;
InterPro: IPR00175; Na/ntran_symport.
Pfam: PF00209; SNF; 1. Nucleoside transport.
PRINTS: PR00176; Nucleoside transport.
ProDom: PD000448; Na/ntran_symport; 1.
DR PROSITE: PS50267; Na_NEUTROTAN_SYM_3; 1.
KW Hypothetical protein.
SQ SEQUENCE 671 AA: 75025 MW: 3A561F5559280C9E CRC64;

Query Match 50.5%; Score 1585.5; DB 5; Length 671;
Best Local Similarity 48.9%; Pred. No. 6.5e-121;
Matches 301; Conservative 110; Mismatches 160; Indels 45; Gaps 11;

9 APTAPPDLPATTAOKSRSVVS-----LTPARQ-----RE 39
43 APTA-SEYMPLSVAKPLTLTVSTSHSIDPNEPIALGSLPTTKGRVAAALRRSSMW 101
40 TWAKKAEPFLAVGAVDGNVWRPPICYONGGAFILPYCVMLFGPLPFLLEALG 99
102 KWATMEFLAVGAVDGNVWRPPICYONGGAFILPYCVMLFGPLPFLLEALG 161
100 OYHRCGCLTLMKRICPALKGVGYAICMIDYMGVNTTIGNAVYYLLASLTI-NSVLP 158
162 OFHRCGCVSVMKRCVPLFRGIGYICICTFATFYMALIAOVFAIVLSKIMDEVP 221
159 WTSCDNEWNTPLCTP---VTSPTNPNSSTPAKEFEERNVLEQHSNGLDDMGPIKPSLA 215
222 WASCNPNMTPRCSDDLNTISRNGTPLTPSEERYLYKVLVOKSTGDDLGKVTSM 281
216 LCPGVFLVYFSLMKGVRSACKVWVATALADYVLLILARGVTLPGATGIRYLLPE 275
282 VCLLAVFIWYFALMKGPSSGKIYVWATATAYIILSILLINGLLPGAKNGLYYVTPD 341
276 WHKLONSKVWIDAASQIFPSLPGFGTLLALSSYKFNPNKYDALITSSINCLTSLAG 335
342 FEKLADPAVWSAAAOIFPSLPGFGVLLALSSYKFNPNKYDALITSSINCLTSLAG 401
336 FVTFVGLVMAHVOKSIEE-VGLEPGGLVFIYVEALATMGVSFWALIFLMLITGL 394
402 CVFSTGLGMSLTLTKPINEVVEGDASLFIYVQALATMDYSCFWSSTIFVMLITGL 461
395 DSTFGLEAVTALCDEYPRVLGRHREVFVAVALLFIYICALPTTYGGVYVLDLNYG 454
462 DSTFGIEAFITGFCDE-SRFLSKRKWVLYICIIYFLSPALSYGGQFVIFPLEDEG 520
455 PELAILFVFAEAGCVWYGVDRPSSEVDRYMLGHTPGWFWTCWSYISPVFLVLFVS 514
521 VLSLFLVITCMIWVWYGVDRPSSEVDRYMLGHTPGWFWTCWSYISPVFLVLFVS 579
515 VL--AHEEMLGEYTYPSMSTIVGWMTGTVCSCPILYIYKLLITPGNCIRIKTIORP 572
580 VYNSFFKPIOMASTYFPMWSVILGWFLRLLSVLAIPVFAIYLLSGTGLYERFWATTP 639

OY 573 E-----VTSIPPADST 583
Db 640 QOORNSATSL-AADPT 654

RESULT 15
O963F3
ID Q963F3 PRELIMINARY; PRT; 671 AA.
AC Q963F3;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Serotonin reuptake transporter.
GN MOD-5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN (1)
RP SEQUENCE FROM N.A.
RA Ranganathan R., Sawin E.R., Trent C., Horvitz R.;
RT "Mutations in the *C. elegans* Serotonin Reuptake Transporter MOD-5
RT Reveal Serotonin-Dependent and -Independent Activities of
RT Fluoxetine.";
RT Submitted (May-2001) to the EMBL/Genbank/DBJ databases.
RL EMBL: AF385631; AAK84832.1;
DR InterPro: IPR00175; Na/ntran_symport.
DR Pfam: PF00209; SNF; 1.
DR ProDom: PD000448; Na/ntran_symport; 1.
DR PROSITE: PS50267; Na_NEUTROTAN_SYM_3; 1.
SQ SEQUENCE 671 AA: 75037 MW: 8C1F180EBC9100A1 CRC64;

Query Match 50.3%; Score 1579.5; DB 5; Length 671;
Best Local Similarity 48.7%; Pred. No. 2e-120;
Matches 300; Conservative 110; Mismatches 161; Indels 45; Gaps 11;

9 APTAPPDLPATTAOKSRSVVS-----LTPARQ-----RE 39
43 APTA-SEYMPLSVAKPLTLTVSTSHSIDPNEPIALGSLPTTKGRVAAALRRSSMW 101
40 TWAKKAEPFLAVGAVDGNVWRPPICYONGGAFILPYCVMLFGPLPFLLEALG 99
102 KWATMEFLAVGAVDGNVWRPPICYONGGAFILPYCVMLFGPLPFLLEALG 161
100 OYHRCGCLTLMKRICPALKGVGYAICMIDYMGVNTTIGNAVYYLLASLTI-NSVLP 158
162 OFHRCGCVSVMKRCVPLFRGIGYICICTFATFYMALIAOVFAIVLSKIMDEVP 221
159 WTSCDNEWNTPLCTP---VTSPTNPNSSTPAKEFEERNVLEQHSNGLDDMGPIKPSLA 215
222 WASCNPNMTPRCSDDLNTISRNGTPLTPSEERYLYKVLVOKSTGDDLGKVTSM 281
216 LCPGVFLVYFSLMKGVRSACKVWVATALADYVLLILARGVTLPGATGIRYLLPE 275
282 VCLLAVFIWYFALMKGPSSGKIYVWATATAYIILSILLINGLLPGAKNGLYYVTPD 341
276 WHKLONSKVWIDAASQIFPSLPGFGTLLALSSYKFNPNKYDALITSSINCLTSLAG 335
342 FEKLADPAVWSAAAOIFPSLPGFGVLLALSSYKFNPNKYDALITSSINCLTSLAG 401
336 FVTFVGLVMAHVOKSIEE-VGLEPGGLVFIYVEALATMGVSFWALIFLMLITGL 394
402 CVFSTGLGMSLTLTKPINEVVEGDASLFIYVQALATMDYSCFWSSTIFVMLITGL 461
395 DSTFGLEAVTALCDEYPRVLGRHREVFVAVALLFIYICALPTTYGGVYVLDLNYG 454
462 DSTFGIEAFITGFCDE-SRFLSKRKWVLYICIIYFLSPALSYGGQFVIFPLEDEG 520
455 PELAILFVFAEAGCVWYGVDRPSSEVDRYMLGHTPGWFWTCWSYISPVFLVLFVS 514
521 VLSLFLVITCMIWVWYGVDRPSSEVDRYMLGHTPGWFWTCWSYISPVFLVLFVS 579
515 VL--AHEEMLGEYTYPSMSTIVGWMTGTVCSCPILYIYKLLITPGNCIRIKTIORP 572

Db	580	VYNSSEFKPIOMASYTFPMWSYTLGWFRLSLVLAIPVFAITYLLSGTGTLYERFRWATP	639
Oy	573	E-----VTSIPPADST	583
Db	640	QQRNSATSL-AADPT	654

Search completed: July 18, 2003, 22:00:33
Job time : 53 secs